

5'	9	18	27	36	45	54
NNG	AAG	GCT	CAG	CAT	ACA	CGT
		CGT	CGT	GAC	TTG	GAA
				CGT	GGC	TTC
					GGC	AGC
						GCC
						CCT
63	72	81	90	99	108	
CGA	GCT	CTC	AGT	GAC	CTG	CTT
						GAC
						ATA
117	126	135	144	153	162	
TAT	GTT	ATT	GGT	TTG	CAG	GAA
						TTG
						AAC
						TCT
						GGG
						ATC
						ATA
						AGC
						CTC
						CTT
						TCC
						GAT
171	180	189	198	207	216	
GCT	GCC	TTT	AAT	GAC	TCG	TGG
						AGC
						AGT
						TTC
						CTC
						ATG
						GAT
						GTG
						CTT
						TCC
						CCT
						CTG
						L
225	234	243	252	261	270	
AGC	TTT	ATC	AAG	GTC	TCC	CAT
						GTC
						ATG
						CAG
						GGG
						ATC
						CTC
						TTA
						CTG
						GTC
						TTT
279	288	297	306	315	324	
GCC	AAG	TAT	CAG	CAT	TTG	CCC
						TAT
						ATC
						CAG
						ATT
						CTG
						TCT
						ACT
						AAA
						TCC
						ACC
						CCC
333	342	351	360	369	378	
ACT	GGC	CTG	TTT	GGG	TAC	TGG
						GGG
						AAC
						AAA
						GGT
						GGA
						GTC
						ATC
						TGC
						CTG
						AAG
						K
						L
						C
						I
						N
						V
						G
						G
						N
						I
						C
						L
						K

FIGURE 1A

387	396	405	414	423	432
CTT TAT GGC TAC TAT GTC AGC ATC AAC TGC CAC CTG CCT CCC CAC ATT TCC					
L Y G Y Y V S I I N C H L P P H I S					
441	450	459	468	477	486
AAC AAT TAC CAG CGG CTG GAG CAC TTT GAC CGG ATC CTG GAG ATG CAG AAT TGT					
N N Y Q R L E H F D R I L E M Q N C					
495	504	513	522	531	540
GAG GGG CGA GAC ATC CCA AAC ATC CTG GAC CAC GAC CTC ATT ATC TGG TTT GGA					
E G R D I P N I L D H D L I I W F G					
549	558	567	576	585	594
GAC ATG AAC TTT CGG ATC GAG GAC TTT GGG TTG CAC TTT GTT GGT CGG GAA TCC ATT					
D M N F R I E D F G L H F V R E S I					
603	612	621	630	639	648
AAA AAT CGG TGC TAC GGT GGC CTG TGG GAG AAG GAC CAG CTC AGC ATT GCC AAG					
K N R C Y G G L W E K D Q L S I A K					
657	666	675	684	693	702
AAA CAT GAC CCG CTG CTC CGG GAG TTC CAG GAG GGC CGC CTA CTC TTC CCG CCC					
K H D P L L R E F Q E G R L L F P P					
711	720	729	738	747	756

FIGURE 1B

ACC TAC AAG TTT GAT AGG AAC TCC AAC GAC TAT GAC ACC AGT GAG AAA AAA CGC	
T Y K F D R N S N D Y D T S E K K R	
765	774
AAG CCT GCA TGG ACC GAT CGC ATC CTG TGG AGG CTG AAG CGG CAG CCC TGT GCT	801
K P A W T D R I L W R L K R Q P C A	810
819	828
GGC CCC GAC ACT CCC ATA CCG CCG GCG TCA CAC TTC TCC TTG TCT CTG AGG GGC	837
G P D T P I P P A S H F S L S L R G	855
873	882
TAC AGC AGC CAC ATG ACG TAC GGC ATC AGC GAC CAC AAG CCT GTC TCC GGC ACG	891
Y S S H M T Y G I S D H K P V S G T	900
927	936
TTC GAC TTG GAG CTG AAG CCA TTG GTG TCT GCT CCG CTG ATC GTC CTG ATG CCC	945
F D L E L K P L V S A P L I V L M P	954
981	990
GAG GAC CTG TGG ACC GTG GAA AAT GAC ATG ATG GTC AGC TAC TCT TCA ACC TCG	999
E D L W T V E N D M M V S Y S S T S	1008
1035	1044
	1053
	1062
	1071
	1080

FIGURE IC

GAC TTC CCC AGC AGC CCG TGG GAC TGG ATT GGA CTG TAC AAG GTG GGG CTG CGG	
D F P S S P W D W I G L Y K V G L R	
1089	1098
GAC GTT AAT GAC TAC GTG TCC TAT GCC TGG GTC GGG GAC AGC AAG GTC TCC TGC	1107
D V N D Y V S Y A W V G D S K V S C	1116
	1125
1143	1152
AGC GAC AAC CTG AAC CAG GTT TAC ATC GAC ATC AGC AAT ATC CCT ACC ACT GAA	1161
S D N L N Q V Y I D I S N I P T T E	1170
	1179
1197	1206
GAT GAG TTT CTC CTC TGT TAC TAC AGC AAC AGT CTG CGT TCT GTG GGG ATA	1215
D E F L L C Y Y S N S L R S V V G I	1224
	1233
1251	1260
AGC AGA CCC TTC CAG ATC CCG CCT GGC TCC TTG AGG GAG GAC CCA CTG GGT GAA	1269
S R P F Q I P P G G L R E D P L G E	1278
	1287
1305	1314
GCA CAG CCA CAG ATC TGA GCC AGG ATG GGA GTG AAT CCC AGG CGG AGG CCA GAG	1323
A Q P Q I	1332
	1341
1359	1368
CTG GCA GCC AGC TCT GCC TTT CCA CTG CCG GGA GTG CTG GGG GCC CAG CCT GGC	1377
	1386
	1395
	1404

FIGURE 1D

1413	1422	1431	1440	1449	1458
CCC CTG AAG AGA CAG CCA AGT GTC GTC CAC ATA CTC CTC CCA GAG TGA GCT CTA					
1467	1476	1485	1494	1503	1512
ACC AGG CTC ATT TGC TCT CTC CAC TAC TCA TCT CTG GAA TTA GCC GCT TAA ATA					
1521	1530	1539	1548	1557	1566
CAG GTT TTT GTT GCT GAG ATG TGA GTG AAA CCA GCT AGT GTG TCA ACA GTG AAG					
1575	1584	1593	1602	1611	1620
ACC TGG GGA CAG TTC TGC GTC TCA TTT CTG GAT TCC TAC CCC CTC TTC TAG TCT					
1629	1638	1647	1656	1665	1674
TGC CCA AGT AGT CCT GCC AGG CAC ATG CCC CAT TTG GCA CAG GCC TGC ATT CTT					
1683	1692	1701	1710	1719	1728
GTC GTG CCG TCC TGG GCC TCA GGC TGT CTG GGA GGG GAG ATG CTC ACA TTT GTA					
1737	1746	1755	1764	1773	1782
CAG GCT ACA TAG ACT GGT GCA AGC AGT GCT GGA TTC CAG GAG TCT TGG CAT CTC					
1791	1800	1809	1818	1827	1836
ATA GCT TGT CCC CGT GAG GAG TGA GCA GAG GGT CTG GGA TTT CTG CTT TCA GCA					

FIGURE 1E

1845	1854	1863	1872	1881	1890
AAA GCA GTC TGA CTC AGT GGG CAG AAT GGA GGG GCC CCT CTA GCC AGG CTC TTA					
1899	1908	1917	1926	1935	1944
CGC CAT GGT TAT GAG CAG GTT GAT GAG GGT CCT TCG GCC AGC ACA ACC TTC CTC					
1953	1962	1971	1980	1989	1998
CCT ACT CAC GGC ATG GAG TCT GAC TGC ATG GAA GTT CCA GAT CCT GAC AGA GAG					
2007	2016	2025	2034	2043	2052
AAC TGG GAA GGA TCC AGG TTC GCT TCC GTT GGT AGC TTG AGT CCC ATG CCT CCA					
2061	2070	2079	2088	2097	2106
CCC TGC CAT CTG AGG AAG GGG TGA CAA GTG GTC AAG GAG CTG TGG CCA CAG ACT					
2115	2124	2133	2142	2151	2160
TTT CCA GGG TGG TCC TTG GCA GGT GAG GTG CGT CTG TGC CAC CCT TGT CAG GAG					
2169	2178	2187	2196	2205	2214
TCA TTG ACG ACG GGC CCC CCC TGG ACC CCC CGG GAC CTC AGA GTG GGG GCA GGC					
2223	2232	2241	2250	2259	2268
AGA AGG GAG AAC CAG CTC AAG ACA TTT TGG AGG ATC TGG CCC TGG GGT TCT TCA					

FIGURE 1F

2277	2286	2295	2304	2313	2322
GAG AAC ACC CTC TAG GGG CTT TGG GGA CAT GGC CTG TCC CCA CAT CCA GCA CTT					
2331	2340	2349	2358	2367	2376
GCC TCC GCC ATG GTC ACT CGG CAG CCC TTT TCC CAG GAG AAG ACA CCT CTG GGA					
2385	2394	2403	2412	2421	2430
GCC TGC TCA GTG CTT GTC CTG CCA TCC TGT GTC CTG GGA CTG AGG GTT ACT CCA					
2439	2448	2457	2466	2475	2484
GTT GCT CTG TGT TGC ATA CTC TCC CCC GCA AGC CTG TGT ATG AAG AAT TGT CCC					
2493	2502	2511	2520	2529	2538
CTG GCT TCC AGC AGG CCA TGG CTG GCT GTT TTG TGA CTG TTA CAT TGT GCA GGG					
2547	2556	2565	2574		
GTA ATT ATT AGC GTG GCT TTT ACA CTT AAA AAA AAA A 3'					

FIGURE 1G

[illegible]

FIGURE 2A

[illegible]

FIGURE 2B

107	D	H	D	L	I	I	W	F	G	D	M	N	F	R	I	E	D	F	G	L	H	F	V	R	E	S	I	K	N	R	C	Y	G	G	L	W	E	K	D	Q	638789	
3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g1399105		
467	N	H	D	V	I	L	W	L	G	D	L	N	Y	R	I	E	E	L	D	V	E	K	V	K	K	L	I	E	E	K	D	F	Q	M	L	Y	A	Y	D	Q	g1019103	
413	K	H	E	V	V	I	W	L	G	D	L	N	Y	R	L	C	M	P	D	A	N	E	V	K	S	L	I	N	K	K	D	L	Q	R	L	L	K	F	D	Q	g1420920	
147	L	S	I	A	K	K	H	D	P	L	L	R	E	F	Q	E	G	R	L	L	F	P	P	T	Y	K	F	D	R	N	S	N	D	Y	D	T	S	E	K	K	638789	
25	L	N	M	A	K	N	T	W	P	I	L	K	G	F	Q	E	G	P	L	N	F	A	P	T	F	K	F	D	V	G	T	N	K	Y	D	T	S	A	K	K	g1399105	
507	L	K	I	Q	V	A	A	K	T	V	F	E	G	F	T	E	G	E	L	T	F	Q	P	T	Y	K	Y	D	T	G	S	D	D	W	D	T	S	E	K	C	g1019103	
453	L	N	I	Q	R	T	Q	K	K	A	F	V	D	F	N	E	G	E	I	K	F	I	P	T	Y	K	Y	D	S	K	T	D	R	W	D	S	S	G	K	C	g1420920	
187	R	K	P	A	W	T	D	R	I	L	W	R	L	K	R	Q	P	C	A	G	P	D	T	P	I	P	P	A	S	H	F	S	L	S	L	R	G	Y	S	S	638789	
65	R	K	P	A	W	T	D	R	I	L	W	K	V	K	-	A	P	G	G	G	P	S	P	S	G	R	K	S	H	R	L	Q	V	T	Q	H	S	Y	R	S	g1399105	
547	R	A	P	A	W	C	D	R	I	L	W	K	G	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g1019103	
493	R	V	P	A	W	C	D	R	I	L	W	R	G	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g1420920	
227	H	M	T	Y	G	I	S	D	H	K	P	V	S	G	T	F	D	L	E	L	K	P	L	V	S	A	P	L	I	V	L	M	P	E	D	L	W	T	V	-	638789	
104	H	M	E	Y	T	V	S	D	H	K	P	V	A	A	Q	F	L	L	Q	F	A	F	R	D	D	M	P	L	V	R	L	E	V	A	D	E	W	V	R	-	g1399105	
570	H	M	A	L	K	T	S	D	H	K	P	V	S	S	V	F	D	I	G	V	R	V	N	D	E	R	L	Y	R	K	T	L	E	E	I	V	R	S	L	D	g1019103	
516	H	M	E	L	K	T	S	D	H	K	P	V	S	A	L	F	H	I	G	V	K	V	V	D	E	R	R	Y	R	K	V	F	E	D	S	V	R	I	M	D	g1420920	
266	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	638789		
143	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g1399105		
610	K	M	E	N	A	N	I	P	S	V	S	L	S	K	R	E	E	F	C	F	Q	N	V	K	Y	M	Q	L	K	V	E	S	F	T	I	-	H	N	G	Q	V	g1019103
556	R	M	E	N	D	F	L	P	S	L	E	L	S	R	R	E	E	F	V	F	E	N	V	K	F	R	Q	L	Q	K	G	K	F	Q	I	S	N	N	G	Q	V	g1420920
300	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	638789		
177	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g1399105		
649	P	C	H	F	E	F	I	N	K	P	D	E	E	S	Y	C	K	Q	W	L	N	A	N	P	S	R	G	F	L	L	P	D	S	D	V	E	I	D	L	E	g1019103	
596	P	C	H	F	S	F	I	P	K	L	N	D	S	Q	Y	C	K	P	W	L	R	A	E	P	F	E	G	Y	L	E	P	N	E	T	V	D	I	S	L	D	g1420920	

FIGURE 2C

317	L N Q V Y I D I S N I P T E D	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	E F	638789
192	T Y Q V T F S E E S L P K G H G	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	D F	g1399105
689	L F V N K T T A T K L N S G E D	K I E D I L V L H L D R G K D Y F L S V S G N Y	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1019103
636	V Y V S K D S V T I L N S G E D	K I E D I L V L H L D R G K D Y F L T I S G N Y	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1420920
335	L L C Y Y S N S L R S V V G I S R P F	- Q I P	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	638789
210	I L G Y Y S H N H S I L I G I T E P F	- Q I S	L P S - S E L A S S T D S S G T	- - - - -	- - - - -	- - - - -	- - - - -	g1399105
729	L P S C F G S P I H T L C Y M R E P	I L D L P	L E T I S E L - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1019103
676	L P S C F G T S L E A L C R M K R P	I R E V P	V T K L I D L E E D S F L E K E K	- - - - -	- - - - -	- - - - -	- - - - -	g1420920
357	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	638789
248	S - - - S E G E D D S T L E - -	L L A P K S R S P S P G K S K R H R S R S P G	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1399105
759	T L M P V W T G D D G S Q L D S P M E I P K E L W M V D Y L Y R N A V Q Q E D	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1019103
716	S L L Q M V P L D E G A S - E R P L Q V P K E I W L L V D H L F K Y A C H Q E D	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1420920
357	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	638789
282	L A R F P G L A - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1399105
799	L F Q Q P G L R S E F E H I R D C L D T G M I D N L S A S N H S V A E A L L L F	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1019103
755	L F Q T P G M Q E E L Q Q I I D C L D T S I P E T I P G S N H S V A E A L L I F	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1420920
357	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	638789
313	R V A - P D R S S N G S S R G S S E E G P S G L P G P W A F P P A V P R S - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1399105
839	L E S L P E P V I C Y S T Y H N C L E C S G N Y T A S K Q V I S T L P I F H K N	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1019103
795	L E A L P E P V I C Y E L Y Q R C L D S A Y D P R I C R Q V I S Q L P R C H R N	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	g1420920
357	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	P G	638789
349	- - - - L G L L P A L - R L E T V D P G G G S W G P D R E A L - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	A P N	g1399105
879	V F H Y L M A F L R E L L K N S A K N H L D E N I L A S I F G S L L L R N P A G	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	A G	g1019103
835	V F R Y L M A F L R E L L K F S E Y N S V N A N M I A T L F T S L L L R P P P N	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	P N	g1420920

FIGURE 2D

Library	Lib Description	Abun	Pct Abun
PANCISM01	pancreas, islet cells, NORM, WM	2	0.1907
SCORNON01	spinal cord, 71 M, NORM	1	0.1379
BSTMNOT01	brain stem, 72 M	1	0.1214
MUSCNOT01	skeletal muscle, WM	2	0.0861
THP1NOT01	THP-1 promonocyte cell line, untreated	1	0.0571
SYNORAT01	synovium, elbow, rheumatoid, 51 F	1	0.0478
NERVMSM01	multiple sclerosis, 46 M, NORM, WM	2	0.0448
BRSTNOT03	breast, 54 F, match to BRSTTUT02	3	0.0441
PENCNOT01	penis, corpus cavernosum, 53 M	1	0.0394
COLNNOT09	colon, 60 M, match to COLNTUT16	1	0.0390
PROSNOT20	prostate, 65 M, match to PROSTUT12	1	0.0336
COLNNOT13	colon, ascending, 28 M	1	0.0311
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293
SCORNOT04	spinal cord, 32 M	1	0.0293
LEUKNOT02	white blood cells, 45 F	1	0.0292
COLNFET02	colon, fetal F	2	0.0286
THYRTUT03	thyroid tumor, benign, 17 M	1	0.0276
LNODNOT05	lymph nodes, 14 F	1	0.0271
THP1AZS08	THP-1 promonocyte cell line, treated AZ, SUB	2	0.0269
UTRSNOT08	uterus, endometrium, 35 F	1	0.0267
HEAANOT01	heart, coronary artery, 46 M	1	0.0265
HEAONOT03	heart, aorta, 27 F	1	0.0265
BRAITUT13	brain tumor, meningioma, 68 M	1	0.0262
COTRNOT01	colon, transverse, Crohn's, 26 M	1	0.0260

FIGURE 3A

BONRFET01	rib, fetal M	1	0.0259
SINTFET03	small intestine, fetal F	2	0.0259
THYMNON04	thymus, 3 M, NORM	1	0.0257
STOMFET01	stomach, fetal F	1	0.0255
TYLMNOT02	lymphocytes (non-adher PBMNC), M/F	1	0.0254
HEAONOT05	heart, aorta, 17 F	1	0.0252
UTRSTUT04	uterine tumor, leiomyoma, 34 F	1	0.0250
LUNGUTUT13	lung tumor, adenocarcinoma, 47 M	1	0.0249
PONSAZT01	brain, pons, Alzheimer's, 74 M	1	0.0249
TMLR3DT02	lymphocytes (non-adher PBMNC), M/F, 72-hr MLR	1	0.0246
PROSNOT15	prostate, 66 M, match to PROSTUT10	1	0.0241
SINJNOT02	small intestine, jejunum, 8 F	1	0.0241
UCMCNOT02	mononuclear cells	1	0.0236
LIVSFEM03	liver/spleen, fetal M, NORM, WM	1	0.0214
BRSTNOM02	breast, F, NORM, WM	1	0.0206
BRSTTUT03	breast tumor, 58 F, match to BRSTNOT05	2	0.0197
COLNTUT03	colon tumor, 62 M, match to COLNNOT16	1	0.0196
THYMNOT02	thymus, 3 M	1	0.0194
HNT3AZT01	hNT2 cell line, teratocarcinoma, treated AZ	1	0.0191
NEUTLPT01	granulocytes, periph blood, M/F, treated LPS	1	0.0173
MUSCNOT07	muscle, forearm, 38 F	1	0.0154
COLNNOT11	colon, 60 M, match to COLNTUT16	1	0.0149
NGANNOT01	ganglioneuroma, 9 M	2	0.0146
PROSTUT05	prostate tumor, 69 M, match to PROSNOT07	1	0.0145
THYRNOT03	thyroid tumor, adenoma, 28 F	1	0.0138
SPLNNOT04	spleen, 2 M	1	0.0128

FIGURE 3B

KIDNNOT05	kidney, neonatal F	1	0.0106
EOSIHET02	eosinophils, hypereosinophilia, 48 M	1	0.0105
OVARTUT01	ovarian tumor, 43 F, match to OVARNOT03	1	0.0103
UTRPNOM01	uterus, F, NORM, WM	1	0.0101
MELANOM01	melanocytes, M, NORM, WM	1	0.0096
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0095
BRAINOM01	brain, infant F, NORM, WM	2	0.0089
CARDFEM01	heart, fetal, NORM, WM	1	0.0082
UTRSNOT02	uterus, 34 F	1	0.0078
LUNGFET03	lung, fetal F	1	0.0069
PLACNOM02	placenta, neonatal F, NORM, WM	1	0.0056
LIVSFEM02	liver/spleen, fetal M, NORM, WM	2	0.0053

FIGURE 3C